APPROVED O.G. FIG.

BY CLASS SUBCLASS

DRAFTSMAN

1/7

GGAGGGCAGCAAGGACGCACCAAGGGAGCTACCCCATGGACAGGGCCCCACAGAGACACCACCGGACAT CTCGGGAGCTGCTGCAAAGAAGACCCACACCTCACAAATTGAAGTGATCCCTTGCAAGATCTGTGG GGACAAGTCATCTGGGATCCACTACGGGGTTATCACCTGTGAGGGGTGCAAGGGCTTCTTCCGCCGCAGC CAGCAGTGTAATGTGGCCTACTCCTGCACGCGTCAGCAGAACTGCCCCATTGACCGAACCAGCCGCAACC GATGCCAGCATTGCCGCCTGCAGAAGTGCCTGGCCTCTGGGCATGTCCCGAGATGCTGTCAAGTTTGGCCG AATGTCCAAGAAGCAGAGGGACAGTCTACATGCAGAAGTGCAGAAACAACTGCAACAGCAGCAGCAACAG CAGATGGGCAGCTACCACTGGGCGCCTCACCTGACCTACCCGAGGCCTCTGCTTGTCCCCCTGGCCTCCT GAGAGCCTCAGGCTCTGGCCCACCATATTCCAATACCTTGGCCAAAACAGAGGTCCAGGGGGCCTCCTGC CACCTTGAGTATAGTCCAGAACGAGGCAAAGCTGAAGGCAGGACAGCATCTATAGCACTGACGGCCAAC TTACTCTTGGAAGATGTGGACTTCGTTTTGAGGAAACCAGGCATCCTGAACTTGGGGAACCAGAACAGGG GAGTACCTGGTACAGAATGTCTGCAAGTCCTTCCGAGAGACATGCCAGCTGCGACTGGAGGACCTTCTAC GGCAGCGCACCAACCTCTTTTCACGGGAGGAGGTGACCAGCTACCAGAGGAAGTCAATGTGGGAGATGTG GGAGCGCTGTGCCCACCACCTCACTGAGGCCATTCAGTATGTGGTGGAGTTTGCCAAGCGGCTTTCAGGC TTCATGGAGCTCTGCCAGAATGACCAGATCATACTACTGACAGCAGGAGCAATGGAAGTCGTCCTAGTCA GAATGTGCAGGGCCTACAATGCCAACAACCACACAGTCTTTTTTGAAGGCAAATACGGTGGTGTGGAGCT GTTTCGAGCCTTGGGCTGCAGCGAGCTCATCAGCTCCATATTTGACTTTTCCCACTTCCTCAGCGCCCTG TGTTTTTCTGAGGATGAGATTGCCCTCTACACGGCCCTGGTTCTCATCAATGCCAACCGTCCTGGGCTCC AAGAGAAGAGGAGAGTGGAACATCTGCAATACAATTTGGAACTGGCTTTCCATCATCATCTCTGCAAGAC TCATCGACAAGGCCTCCTAGCCAAGCTGCCACCCAAAGGAAAACTCCGGAGCCTGTGCAGCCAACATGTG GAAAAGCTGCAGATCTTCCAGCACCTCCACCCCATCGTGGTCCAAGCCGCCTTCCCNCCACTCTATAAGG TTTCCTTCAGCCCTCTGACCCGTCTCCCTGGACTCCCTTCACCCAGCCTTTCCCCTTTCTGCACTCTATGA AGGGTGGTATCCCTAGGAGTAAGCAAATCCTAAGACTGATTTTCTGCCCCTAGGCTTGCCTTGTAGGACA ACAGCAGCAAGTGATGGAAAAAGGCTTGTTATGTTTGATTTCCCATAAGTTCCACCCTGGCTTCTGGAA GCTGTGGGGTAGATGGGATAGGATAGGATGACCAAGTCAAATAAAAAACAGACTGACAATCAGCAGGGA TAAATCCAGGTACCTGGGATAAGGAGAACTCAAATCTAGGCTTGAAAGCTAATAACAGTCCTTTCAATAC CTCATTGTATTTCCCCATGGGTCCTCCTGGGGGGACATGGATCTAGCTCAGAGACTGGTGGCAAGCCCCC AGAAGGACCTGTATATAATAAGAATATAGATTCCTG (SEQ ID NO:1)

MDRAPQRHHRTSRELLAAKKTHTSQIEVIPCKICGDKSSGIHYGVITCEGCKGFFRRSQQCN VAYSCTRQQNCPIDRTSRNRCQHCRLQKCLALGMSRDAVKFGRMSKKQRDSLHAEVQKQ LQQQQQEQVAKTPPAGSRGADTLTYTLGLSDGQLPLGASPDLPEASACPPGLLRASGSGPP YSNTLAKTEVQGASCHLEYSPERGKAEGRDSIYSTDGQLTLGRCGLRFEETRHPELGEPEQG PDSHCIPSFCSAPEVPYASLTDIEYLVQNVCKSFRETCQLRLEDLLRQRTNLFSREEVTSYQR KSMWEMWERCAHHLTEAIQYVVEFAKRLSGFMELCQNDQIILLTAGAMEVVLVRMCRAY NANNHTVFFEGKYGGVELFRALGCSELISSIFDFSHFLSALCFSEDEIALYTALVLINANRPGL QEKRRVEHLQYNLELAFHHHLCKTHRQGLLAKLPPKGKLRSLCSQHVEKLQIFQHLHPIVV QAAFPPLYKELFSTDVESPEGLSK (SEQ ID NO:2)

APPROVED O.G. FIG.

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underlined = deleted in targeting construct

[] = sequence flanking Neo insert in targeting construct

GGAGGCCACCAAGGCACCAAGGGAGCTACCCCATGGACAGGGCCCCACAGAGACAC CACCGGACATCTCGGGAGCTGCTGGCTGCAAAGAAGACCCACACCTCACAAATTGAAGTG ATCCCTTGCAAGATCTGTGGGGACAAGTCATCTGGGATCCACTACGGGGTTATCACCTGT GAGGGGTGCAAG [GGCTTCTTCCGCCGCAGCCAGCAGTGTAATGTGGCCTACTCCTGCACG CGTCAGCAGAA] CTGCCCCATTGACCGAACCAGCCGCAACCGATGCCAGCATTGCCGCCTG CAGAAGTGCCTGGCTCTGGGCATGTCCCGAGATGCTGTCAAGTTTGGCCGAATGTCCAAG AAGCAGAGGGACAGTCTACATGCAGAAGTGCAGAAACAACTGCAACAGCAGCAGCAACAG GAACAAGTGGCCAAGACTCCTCCAGCTGGGAGCCGCGGAGCAGACACTTA [CATACACT TTAGGGCTCTCAGATGGGCAGCTACCACTGGGCGCCTCACCTGACCTACCCGAGGCCTCT GCTTGTCCCCCTGGCCTCCTGAGAGCCTCAGGCTCTGGCCCACCATATTCCAATACCTTG GCCAAAACAGAGGTCCAGGGGGCCTCCTGCCACCTTGAGTATAGTCCAGAACGAGGCAAA GCTGAAGGCAGAGACATCTATAGCACTGACGGCCAACTTACTCTTGGAAGATGTGGA CTTCGTTTTGAGGAAACCAGGCATCCTGAACTTGGGGAACCAGAACAGGGTCCAGACAGC G] AGTACCTGGTACAGAATGTCTGCAAGTCCTTCCGAGAGACATGCCAGCTGCGACTGGAG GACCTTCTACGGCAGCGCACCAACCTCTTTTCACGGGAGGAGGTGACCAGCTACCAGAGG AAGTCAATGTGGGAGATGTGGGAGCCCTGTGCCCACCACCTCACTGAGGCCATTCAGTAT GTGGTGGAGTTTGCCAAGCGGCTTTCAGGCTTCATGGAGCTCTGCCAGAATGACCAGATC ATACTACTGACAGGAGGAATGGAAGTCGTCCTAGTCAGAATGTGCAGGGCCTACAAT GCCAACAACCACACTCTTTTTGAAGGCAAATACGGTGGTGTGGAGCTGTTTCGAGCC TTGGGCTGCAGCGAGCTCATCAGCTCCATATTTGACTTTTCCCACTTCCTCAGCGCCCTG TGTTTTTCTGAGGATGAGATTGCCCTCTACACGGCCCTGGTTCTCATCAATGCCAACCGT CCTGGGCTCCAAGAGAGAGAGGAGAGTGGAACATCTGCAATACAATTTGGAACTGGCTTTC CATCATCATCTCTGCAAGACTCATCGACAAGGCCTCCTAGCCAAGCTGCCACCCAAAGGA AAACTCCGGAGCCTGTGCAGCCAACATGTGGAAAAGCTGCAGATCTTCCAGCACCTCCAC CCCATCGTGGTCCAAGCCGCCTTCCCNCCACTCTATAAGGAACTCTTCAGCACTGATGTT CCCTCTGACCCGTCTCCCTGGACTCCCTTCACCCAGCCTTTCCCCTTTCTGCACTCTATGA AGGGTGGTATCCCTAGGAGTAAGCAAATCCTAAGACTGATTTTCTGCCCCTAGGCTTGCC TTGTAGGACAACAGCAGCAAGTGATGGAGAAAAGGCTTGTTATGTTTGATTTCCCATAAG TTCCACCCTGGCTTCTGGAAGCTGTGGGGTAGATGGGATAGGATAGGATGACCAAGTCA AATAAAAACAGACTGACAATCAGCAGGGATAAATCCAGGTACCTGGGATAAGGAGAACT CAAATCTAGGCTTGAAAGCTAATAACAGTCCTTTCAATACCTCATTGTATTTCCCCATGG GTCCTCCTGGGGGGACATGGATCTAGCTCAGAGACTGGTGGCAAGCCCCCAGAAGGACCT GTATATAATAAGAATATAGATTCCTG (SEQ ID NO:1)

## **FIGURE 2A**

Gene Sequence Structure \*

Size of full-length cDNA: 2066 bp

252 bp Sequence Deleted 472 bp

Targeting Vector\* (genomic sequence)

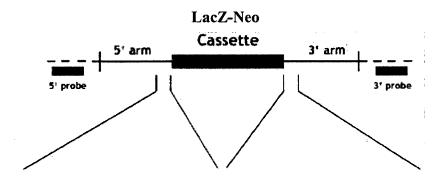
Construct Number: 651

Arm Length:

5': 1.6 kb 3': 2.5 kb

Targeting Vector
- - - - Endogenous Locus

\* Not drawn to scale



5'>CAGGGTCCATCACAATTATAC
AGTGGAGGTTCGGGGACTTTGGTG
GATGTAGAAATTCTTGAGACCAGT
GCACATGAATTGGAGGTCCCTGGG
ACCACCTCAAACTCCGAGAGGGTG
GGATAAGCAGTTTCTGTTTCCCAG
GGCTTCTTCCGCCGCAGCCAGCAG
TGTAATGTGGCCTACTCCTGCACG
CGTCAGCAGAA<3'

(SEQ ID NO:3)

5'>CATACACTTTAGGGCTCTCAG ATGGGCAGCTACCACTGGGCGCCT CACCTGACCTACCCGAGGCCTCTG CTTGTCCCCCTGGCCTCCTGAGAG CCTCAGGCTCTGGCCACCATATT CCAATACCTTGGCCAAAACAGAGG TCCAGGGGGCCTCCTGCCACCTTG AGTATAGTCCAGAACGAGGCAAAG CTGAAGGCAGA<

(SEQ ID NO:4)

FIGURE 2B

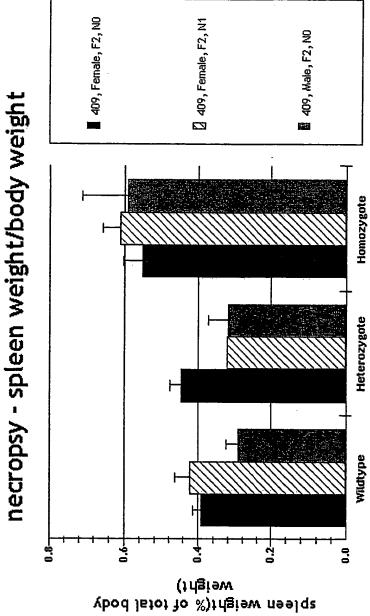


FIG. 3

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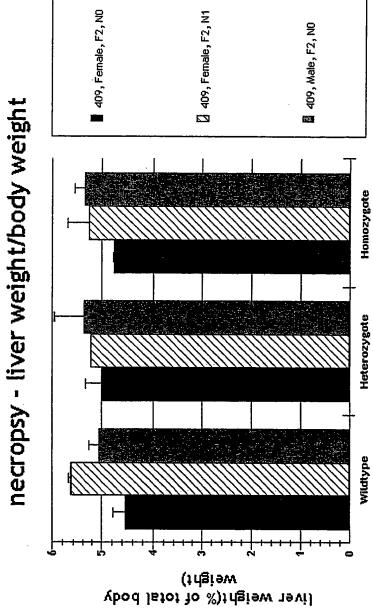
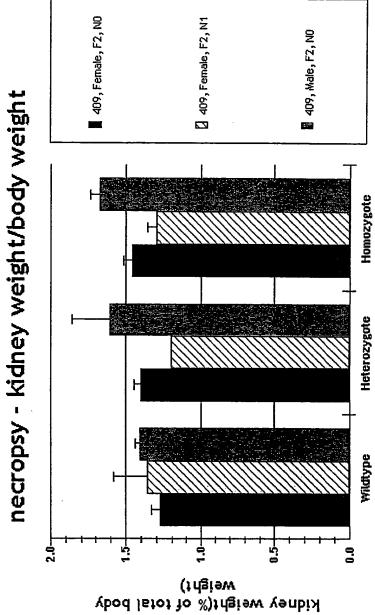


FIG. 4

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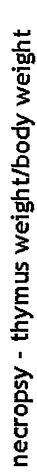


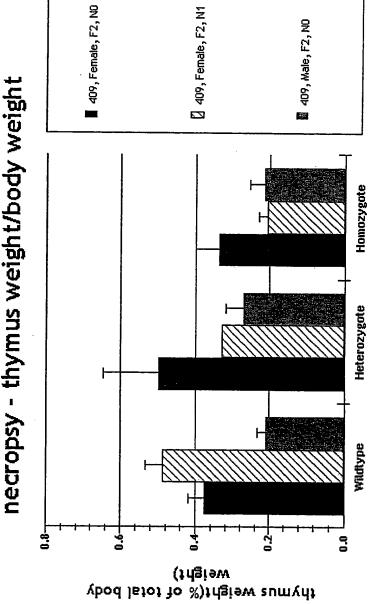


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FIG. 5

ogesta.c.e.e.e





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